



SEQUENCE LISTING

<110> DAI, KEN-SHWO

<120> HUMAN SCII-RELATED GENE VARIANTS ASSOCIATED WITH CANCERS

<130> U 014799-1

<140> 10/653,685

<141> 2003-09-02

<160> 6

<170> PatentIn version 3.2

<210> 1

<211> 1997

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (63)..(1574)

<400> 1
cggggaggaa tatgctgtgg agtcctctg ccatataaac aaaaagagga aatctttcaa 60
ac atg gct gaa gca aag acc cac tgg ctt gga gca gcc ctg tct ctt 107
Met Ala Glu Ala Lys Thr His Trp Leu Gly Ala Ala Leu Ser Leu
1 5 10 15
atc cct tta att ttc ctc atc tct ggg gct gaa gca gct tca ttt cag 155
Ile Pro Leu Ile Phe Leu Ile Ser Gly Ala Glu Ala Ala Ser Phe Gln
20 25 30
aga aac cag ctg ctt cag aaa gaa cca gac ctc agg ttg gaa aat gtc 203
Arg Asn Gln Leu Leu Gln Lys Glu Pro Asp Leu Arg Leu Glu Asn Val
35 40 45
caa aag ttt ccc agt cct gaa atg atc agg gct ttg gag tac ata gaa 251
Gln Lys Phe Pro Ser Pro Glu Met Ile Arg Ala Leu Glu Tyr Ile Glu
50 55 60
aac ccc ttt aaa cgc aca aat gaa ata gtg gag gaa caa tat act cct 299
Asn Pro Phe Lys Arg Thr Asn Glu Ile Val Glu Glu Gln Tyr Thr Pro
65 70 75
caa agc ctt gct aca ttg gaa tct gtc ttc caa gag ctg ggg aaa ctg 347
Gln Ser Leu Ala Thr Leu Glu Ser Val Phe Gln Glu Leu Gly Lys Leu
80 85 90 95
aca gga cca aac aac cag aaa cgt gag agg atg gat gag gaa caa aaa 395
Thr Gly Pro Asn Asn Gln Lys Arg Glu Arg Met Asp Glu Glu Gln Lys
100 105 110
ctt tat acg gat gat gaa gat gat atc tac aag gct aat aac att gcc 443
Leu Tyr Thr Asp Asp Glu Asp Asp Ile Tyr Lys Ala Asn Asn Ile Ala
115 120 125
tat gaa gat gtg gtc ggg gga gaa gac tgg aac cca gta gag gag aaa 491

Tyr	Glu	Asp	Val	Val	Gly	Gly	Glu	Asp	Trp	Asn	Pro	Val	Glu	Glu	Lys	
130					135						140					
ata	gag	agt	caa	acc	cag	gaa	gag	gtg	aga	gac	agc	aaa	gag	aat	ata	539
Ile	Glu	Ser	Gln	Thr	Gln	Glu	Glu	Val	Arg	Asp	Ser	Lys	Glu	Asn	Ile	
145					150						155					
gga	aaa	aat	gaa	caa	atc	aac	gat	gag	atg	aaa	cgc	tca	ggg	cag	ctt	587
Gly	Lys	Asn	Glu	Gln	Ile	Asn	Asp	Glu	Met	Lys	Arg	Ser	Gly	Gln	Leu	
160					165					170					175	
ggc	atc	cag	gaa	gaa	gat	ctt	cgg	aaa	gag	agt	aaa	gac	caa	ctc	tca	635
Gly	Ile	Gln	Glu	Glu	Asp	Leu	Arg	Lys	Glu	Ser	Lys	Asp	Gln	Leu	Ser	
180					185					190						
gat	gat	gtc	tcc	aaa	gta	att	gcc	tat	ttg	aaa	agg	tta	gta	aat	gct	683
Asp	Asp	Val	Ser	Lys	Val	Ile	Ala	Tyr	Leu	Lys	Arg	Leu	Val	Asn	Ala	
195					200					205						
gca	gga	agt	ggg	agg	tta	cag	aat	ggg	caa	aat	ggg	gaa	agg	gcc	acc	731
Ala	Gly	Ser	Gly	Arg	Leu	Gln	Asn	Gly	Gln	Asn	Gly	Glu	Arg	Ala	Thr	
210					215					220						
agg	ctt	ttt	gag	aaa	cct	ctt	gat	tct	cag	tct	att	tat	cag	ctg	att	779
Arg	Leu	Phe	Glu	Lys	Pro	Leu	Asp	Ser	Gln	Ser	Ile	Tyr	Gln	Leu	Ile	
225					230					235						
gaa	atc	tca	agg	aat	tta	cag	ata	ccc	cca	gaa	gac	tta	att	gag	atg	827
Glu	Ile	Ser	Arg	Asn	Leu	Gln	Ile	Pro	Pro	Glu	Asp	Leu	Ile	Glu	Met	
240					245					250					255	
ctc	aaa	act	ggg	gag	aag	ccg	aat	gga	tca	gtg	gaa	ccg	gag	ccg	gag	875
Leu	Lys	Thr	Gly	Glu	Lys	Pro	Asn	Gly	Ser	Val	Glu	Pro	Glu	Arg	Glu	
260					265					270						
ctt	gac	ctt	cct	gtt	gac	cta	gat	gac	atc	tca	gag	gct	gac	tta	gac	923
Leu	Asp	Leu	Pro	Val	Asp	Leu	Asp	Asp	Ile	Ser	Glu	Ala	Asp	Leu	Asp	
275					280					285						
cat	cca	gac	ctg	ttc	caa	aat	agg	atg	ctc	tcc	aag	agt	ggc	tac	cct	971
His	Pro	Asp	Leu	Phe	Gln	Asn	Arg	Met	Leu	Ser	Lys	Ser	Gly	Tyr	Pro	
290					295					300						
aaa	aca	cct	ggt	gct	ggg	act	gag	gcc	cta	cca	gac	ggg	ctc	agt		1019
Lys	Thr	Pro	Gly	Arg	Ala	Gly	Thr	Glu	Ala	Leu	Pro	Asp	Gly	Leu	Ser	
305					310					315						
gtt	gag	gat	att	tta	aat	ctt	tta	ggg	atg	gag	agt	gca	gca	aat	cag	1067
Val	Glu	Asp	Ile	Leu	Asn	Leu	Leu	Gly	Met	Glu	Ser	Ala	Ala	Asn	Gln	
320					325					330					335	
aaa	acg	tcg	tat	ttt	ccc	aat	cca	tat	aac	cag	gag	aaa	gtt	ctg	cca	1115
Lys	Thr	Ser	Tyr	Phe	Pro	Asn	Pro	Tyr	Asn	Gln	Glu	Lys	Val	Leu	Pro	
340					345					350						
agg	ctc	cct	tat	ggt	gct	gga	aga	tct	aga	tcg	aac	cag	ctt	ccc	aaa	1163
Arg	Leu	Pro	Tyr	Gly	Ala	Gly	Arg	Ser	Arg	Ser	Asn	Gln	Leu	Pro	Lys	
355					360					365						
gct	gcc	tgg	att	cca	cat	gtt	gaa	aac	aga	cag	atg	gca	tat	gaa	aac	1211
Ala	Ala	Trp	Ile	Pro	His	Val	Glu	Asn	Arg	Gln	Met	Ala	Tyr	Glu	Asn	

370	375	380	
ctg aac gac aag gat caa gaa tta ggt gag tac ttg gcc agg atg cta			1259
Leu Asn Asp Lys Asp Gln Glu Leu Gly Glu Tyr Leu Ala Arg Met Leu			
385	390	395	
gtt aaa tac cct gag atc att aat tca aac caa gtg aag cga gtt cct			1307
Val Lys Tyr Pro Glu Ile Ile Asn Ser Asn Gln Val Lys Arg Val Pro			
400	405	410	415
ggt caa ggc tca tct gaa gat gac ctg cag gaa gag gaa caa att gag			1355
Gly Gln Gly Ser Ser Glu Asp Asp Leu Gln Glu Glu Glu Gln Ile Glu			
420	425	430	
cag gcc atc aaa gag cat ttg aat caa ggc agc tct cag gag act gac			1403
Gln Ala Ile Lys Glu His Leu Asn Gln Gly Ser Ser Gln Glu Thr Asp			
435	440	445	
aag ctg gcc ccg gtg agc aaa agg ttc cct gtg ggg ccc ccg aag aat			1451
Lys Leu Ala Pro Val Ser Lys Arg Phe Pro Val Gly Pro Pro Lys Asn			
450	455	460	
gat gat acc cca aat agg cag tac tgg gat gaa gat ctg tta atg aaa			1499
Asp Asp Thr Pro Asn Arg Gln Tyr Trp Asp Glu Asp Leu Leu Met Lys			
465	470	475	
gtg ctg gaa tac ctc aat caa gaa aag gca gaa aag gga agg gag cat			1547
Val Leu Glu Tyr Leu Asn Gln Glu Lys Ala Glu Lys Gly Arg Glu His			
480	485	490	495
att gct aag aga gca atg gaa aat atg taagctgctt tcattaatta			1594
Ile Ala Lys Arg Ala Met Glu Asn Met			
500			
ccctactttc attcctccca ccccaagcaa atcccaacat ttctcttcag tgtgttgact			1654
tctatcctgt taacactgta atatcttaa atgatgtaca ggcagatgaa accaggtcac			1714
tggggagtct gcttcatttc ctctgagctg ttatcttgc tatggatatg tgtaaatgtt			1774
atgactcctt gataaaaaat ttattatgtc cattattcaa gaaagatatc tatgactgtg			1834
tttaatagta tatctaattgg ctgtggcatt gttgatgctc acatatgata aaaaagtgtc			1894
ctataattct attgaaagtt tttaatattt attgaattat ttgttactg tctgttagcgt			1954
tttggagt actggaccaa aaaaataaag cattataaat ata			1997

<210> 2
 <211> 504
 <212> PRT
 <213> Homo sapiens
 <400> 2

Met Ala Glu Ala Lys Thr His Trp Leu Gly Ala Ala Leu Ser Leu Ile
 1 5 10 15

Pro Leu Ile Phe Leu Ile Ser Gly Ala Glu Ala Ala Ser Phe Gln Arg

20

25

30

Asn Gln Leu Leu Gln Lys Glu Pro Asp Leu Arg Leu Glu Asn Val Gln
35 40 45

Lys Phe Pro Ser Pro Glu Met Ile Arg Ala Leu Glu Tyr Ile Glu Asn
50 55 60

Pro Phe Lys Arg Thr Asn Glu Ile Val Glu Glu Gln Tyr Thr Pro Gln
65 70 75 80

Ser Leu Ala Thr Leu Glu Ser Val Phe Gln Glu Leu Gly Lys Leu Thr
85 90 95

Gly Pro Asn Asn Gln Lys Arg Glu Arg Met Asp Glu Glu Gln Lys Leu
100 105 110

Tyr Thr Asp Asp Glu Asp Asp Ile Tyr Lys Ala Asn Asn Ile Ala Tyr
115 120 125

Glu Asp Val Val Gly Gly Glu Asp Trp Asn Pro Val Glu Glu Lys Ile
130 135 140

Glu Ser Gln Thr Gln Glu Glu Val Arg Asp Ser Lys Glu Asn Ile Gly
145 150 155 160

Lys Asn Glu Gln Ile Asn Asp Glu Met Lys Arg Ser Gly Gln Leu Gly
165 170 175

Ile Gln Glu Glu Asp Leu Arg Lys Glu Ser Lys Asp Gln Leu Ser Asp
180 185 190

Asp Val Ser Lys Val Ile Ala Tyr Leu Lys Arg Leu Val Asn Ala Ala
195 200 205

Gly Ser Gly Arg Leu Gln Asn Gly Gln Asn Gly Glu Arg Ala Thr Arg
210 215 220

Leu Phe Glu Lys Pro Leu Asp Ser Gln Ser Ile Tyr Gln Leu Ile Glu
225 230 235 240

Ile Ser Arg Asn Leu Gln Ile Pro Pro Glu Asp Leu Ile Glu Met Leu
245 250 255

Lys Thr Gly Glu Lys Pro Asn Gly Ser Val Glu Pro Glu Arg Glu Leu
260 265 270

Asp Leu Pro Val Asp Leu Asp Asp Ile Ser Glu Ala Asp Leu Asp His
275 280 285

Pro Asp Leu Phe Gln Asn Arg Met Leu Ser Lys Ser Gly Tyr Pro Lys
290 295 300

Thr Pro Gly Arg Ala Gly Thr Glu Ala Leu Pro Asp Gly Leu Ser Val
305 310 315 320

Glu Asp Ile Leu Asn Leu Leu Gly Met Glu Ser Ala Ala Asn Gln Lys
325 330 335

Thr Ser Tyr Phe Pro Asn Pro Tyr Asn Gln Glu Lys Val Leu Pro Arg
340 345 350

Leu Pro Tyr Gly Ala Gly Arg Ser Arg Ser Asn Gln Leu Pro Lys Ala
355 360 365

Ala Trp Ile Pro His Val Glu Asn Arg Gln Met Ala Tyr Glu Asn Leu
370 375 380

Asn Asp Lys Asp Gln Glu Leu Gly Glu Tyr Leu Ala Arg Met Leu Val
385 390 395 400

Lys Tyr Pro Glu Ile Ile Asn Ser Asn Gln Val Lys Arg Val Pro Gly
405 410 415

Gln Gly Ser Ser Glu Asp Asp Leu Gln Glu Glu Glu Gln Ile Glu Gln
420 425 430

Ala Ile Lys Glu His Leu Asn Gln Gly Ser Ser Gln Glu Thr Asp Lys
435 440 445

Leu Ala Pro Val Ser Lys Arg Phe Pro Val Gly Pro Pro Lys Asn Asp
450 455 460

Asp Thr Pro Asn Arg Gln Tyr Trp Asp Glu Asp Leu Leu Met Lys Val
465 470 475 480

Leu Glu Tyr Leu Asn Gln Glu Lys Ala Glu Lys Gly Arg Glu His Ile
485 490 495

Ala Lys Arg Ala Met Glu Asn Met
500

<210> 3
 <211> 2077
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (63)..(356)

<400> 3	60
cggggaggaa tatgctgtgg agtcctctg ccatataaac aaaaagagga aatctttcaa	
ac atg gct gaa gca aag acc cac tgg ctt gga gca gcc ctg tct ctt	107
Met Ala Glu Ala Lys Thr His Trp Leu Gly Ala Ala Leu Ser Leu	
1 5 10 15	
atc cct tta att ttc ctc atc tct ggg gct gaa gca gct tca ttt cag	155
Ile Pro Leu Ile Phe Leu Ile Ser Gly Ala Glu Ala Ala Ser Phe Gln	
20 25 30	
aga aac cag ctg ctt cag aaa gaa cca gac ctc agg ttg gaa aat gtc	203
Arg Asn Gln Leu Leu Gln Lys Glu Pro Asp Leu Arg Leu Glu Asn Val	
35 40 45	
caa aag ttt ccc agt cct gaa atg atc agg gct ttg gag tac ata gaa	251
Gln Lys Phe Pro Ser Pro Glu Met Ile Arg Ala Leu Glu Tyr Ile Glu	
50 55 60	
aac ctc cgacaa gct cat aag aaa gaa agc tta agc aca tgc aat	299
Asn Leu Arg Gln Gln Ala His Lys Lys Glu Ser Leu Ser Thr Cys Asn	
65 70 75	
tcc ctc cta tgt atg aag aga att cca ggg ata acc cct tta aac gca	347
Ser Leu Leu Cys Met Lys Arg Ile Pro Gly Ile Thr Pro Leu Asn Ala	
80 85 90 95	
caa atg aaa tagtggagga acaatatact cctcaaagcc ttgctacatt	396
Gln Met Lys	
ggaatctgtc ttccaagagc tggggaaact gacaggacca aacaaccaga aacgtgagag	456
gatggatgag gagcaaaaac ttatacggg ttagatggat gatatctaca aggctaataa	516
cattgcctat gaagatgtgg tcgggggaga agactggAAC ccagtagagg agaaaaataga	576
gagtcaaacacc caggaagagg tgagagacag caaagagaat ataggaaaaa atgaacaaat	636
caacgatgag atgaaacgct cagggcagct tggcatccag gaagaagatc ttccggaaaga	696
gagtaaagac caactctcag atgatgtctc caaagtaatt gcctatttga aaaggtagt	756
aaatgctgca ggaagtggga gtttacagaa tggcaaaat gggaaaggg ccaccaggct	816
ttttgagaaa cctcttgatt ctcagtctat ttatcagctg attgaaatct caaggaattt	876
acagataaccc ccagaagact taattgagat gctcaaaact ggggagaagc cgaatggatc	936
agtggAACCG gagcgggagc ttgaccttcc tggatggatc gatgacatct cagaggctga	996

cttagaccat ccagacctgt	tccaaaatag gatgctctcc	aagagtggct accctaaaac	1056
acctggcgt gctggactg	aggccctacc agacgggctc	agtgttggagg atatttaaa	1116
tcttttaggg atggagagtg	cagcaaatca gaaaacgtcg	tatccatataa	1176
ccaggagaaa gttctgccaa	ggctccctta tggctgctgga	agatctagat cgaaccagct	1236
tcccaaagct gcctggattc	cacatgttga aaacagacag	atggcatatg aaaacctgaa	1296
cgacaaggat caagaattag	gtgagttactt ggccaggatg	ctagttaat accctgagat	1356
cattaattca aaccaagtga	agcgagttcc tggtcaaggc	tcatctgaag atgacctgca	1416
ggaagagggaa caaattgagc	aggccatcaa agagcattt	aatcaaggca gctctcagga	1476
gactgacaag ctggccccgg	ttagcaaaaag gttccctgtg	gggccccgaa agaatgatga	1536
taccccaaat aggcatgtact	ggatgaaga tctgttaatg	aaagtgcgtt aatacctcaa	1596
tcaagaaaag gcagaaaagg	gaaggggagca tattgctaag	agagcaatgg aaaatatgt	1656
agctgcttcc attaattacc	ctactttcat tcctccacc	ccaagcaaat cccaacattt	1716
ctcttcagtg tggacttc	tatcctgtta acactgtaat	atctttaat gatgtacagg	1776
cagatgaaac caggtcactg	gggagtctgc ttcatttcct	ctgagctgtt atcttgcgt	1836
tggatatgtg taaatgttat	gactccttga taaaaaattt	attatgtcca ttattcaaga	1896
aagatatcta tgactgtgtt	taatagtata tctaattggct	gtggcattgt ttagtgcac	1956
atatgataaa aaagtgcct	ataattctat tgaaagttt	taatatttat tgaattattt	2016
tgttactgtc ttagcgttt	tgtggagttac tggaccaaaa	aaataaagca ttataaataat	2076
a			2077

<210> 4
 <211> 98
 <212> PRT
 <213> Homo sapiens

<220>
 <223> UNKNOWN

<400> 4

Met Ala Glu Ala Lys Thr His Trp Leu Gly Ala Ala Leu Ser Leu Ile
 1 5 10 15

Pro Leu Ile Phe Leu Ile Ser Gly Ala Glu Ala Ala Ser Phe Gln Arg
 20 25 30

Asn Gln Leu Leu Gln Lys Glu Pro Asp Leu Arg Leu Glu Asn Val Gln
 35 40 45

Lys Phe Pro Ser Pro Glu Met Ile Arg Ala Leu Glu Tyr Ile Glu Asn
50 55 60

Leu Arg Gln Gln Ala His Lys Lys Glu Ser Leu Ser Thr Cys Asn Ser
65 70 75 80

Leu Leu Cys Met Lys Arg Ile Pro Gly Ile Thr Pro Leu Asn Ala Gln
85 90 95

Met Lys

<210> 5
<211> 1803
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (63)..(539)

<400> 5
cggggaggaa tatgctgtgg agctcctctg ccatataaac aaaaagagga aatctttcaa 60
ac atg gct gaa gca aag acc cac tgg ctt gga gca gcc ctg tct ctt 107
Met Ala Glu Ala Lys Thr His Trp Leu Gly Ala Ala Leu Ser Leu
1 5 10 15
atc cct tta att ttc ctc atc tct ggg gct gaa gca gct tca ttt cag 155
Ile Pro Leu Ile Phe Leu Ile Ser Gly Ala Glu Ala Ala Ser Phe Gln
20 25 30
aga aac cag ctg ctt cag aaa gaa cca gac ctc agg ttg gaa aat gtc 203
Arg Asn Gln Leu Leu Gln Lys Glu Pro Asp Leu Arg Leu Glu Asn Val
35 40 45
caa aag ttt ccc agt cct gaa atg atc agg gct ttg gag tac ata gaa 251
Gln Lys Phe Pro Ser Pro Glu Met Ile Arg Ala Leu Glu Tyr Ile Glu
50 55 60
aac ctc cga caa caa gct cat aag gaa gac agc agc cca gat tat aat 299
Asn Leu Arg Gln Gln Ala His Lys Glu Glu Ser Ser Pro Asp Tyr Asn
65 70 75
ccc tac caa ggt gtc tct gtc ccc ctt cag caa aaa gaa aat ggc gat 347
Pro Tyr Gln Gly Val Ser Val Pro Leu Gln Gln Lys Glu Asn Gly Asp
80 85 90 95
gaa agc cac ttg ccc gag agg gat tca ctg agt gaa gaa gac tgg atg 395
Glu Ser His Leu Pro Glu Arg Asp Ser Leu Ser Glu Glu Asp Trp Met
100 105 110
aga ata ata ctc gaa gct ttg aga cag gct gaa aat gag cct cag tct 443
Arg Ile Ile Leu Glu Ala Leu Arg Gln Ala Glu Asn Glu Pro Gln Ser
115 120 125

gca cca aaa gaa aat aag ccc tat gcc ttg aat tca gaa aag aac ttt	491
Ala Pro Lys Glu Asn Lys Pro Tyr Ala Leu Asn Ser Glu Lys Asn Phe	
130 135 140	
cca atg gac atg agt gat gat tat gag aca cag cag tgg cca gaa aga	539
Pro Met Asp Met Ser Asp Asp Tyr Glu Thr Gln Gln Trp Pro Glu Arg	
145 150 155	
aagcttaagc acatgcaatt ccctcctatg tatgaagaga attccagggtaaacccttt	599
aaacgcacaa atgaaatagt ggaggaacaa tatactcctc aaagccttgc tacattggaa	659
tctgtcttcc aagagctggg gaaactgaca ggaccaaaca accagaaacg tgagaggatg	719
gatgaggagc aaaaacttta tacggatgat gaagatgata tctacaaggc taataacatt	779
gcctatgaag atgtggtcgg gggagaagac tggaacccag tagaggagaa aatagagagt	839
caaaccagg aagaggtgag agacagcaa gagaatata gaaaaaatga acaaatacAAC	899
gatgagatga aacgctcagg gcagcttggc atccaggaag aagatctcg gaaagagagt	959
aaagaccaac tctcagatga tgtctccaaa gtaattgcct atttgaaaag gtttagtaat	1019
gctgcaggaa gtgggagggtt acagaatggg caaaatgggaaagggccac caggctttt	1079
gagaaacctc ttgattctca gtcttattt cagctgattt gaaatctcaag gaatttacag	1139
atacccccaag aagacttaat tgagatgctc aaaactgggg agaagccgaa tggatcagt	1199
gaaccggagc gggagcttga ctttcctttt gacctagatg acatctcaga ggctgactta	1259
gaccatccag acctgttcca aaataggatg ctctccaaga gtggctaccc taaaacaccc	1319
ggctgtgtg ggactgaggc cttaccagac gggctcagtg ttgaggatat tttaatctt	1379
tttagggatgg agagtgcagc aaatcagaaa acgtcgattt ttcccaagca aatcccaaca	1439
tttctttca gtgtgttgc ttctatcctt ttaacactgt aatatcttta aatgtatgtac	1499
aggcagatga aaccaggtca ctggggagtc tgcttcattt cctctgagct gttatcttgc	1559
gtatggatat gtgtaaatgt tatgactct tgataaaaaa ttattatgt ccattattca	1619
agaaaagatat ctatgactgt gtttaatagt atatcta atg gctgtggcat tggatgt	1679
cacatatgt aaaaagtgt cttataattt tattgaaagt tttaatattt tattgaaattt	1739
ttttgttact gtctgttagcg ttttggag tactggacca aaaaataaaa gcattataaa	1799
tata	1803

<210> 6
 <211> 159
 <212> PRT
 <213> Homo sapiens

 <220>
 <223> UNKNOWN

<400> 6

Met Ala Glu Ala Lys Thr His Trp Leu Gly Ala Ala Leu Ser Leu Ile
1 5 10 15

Pro Leu Ile Phe Leu Ile Ser Gly Ala Glu Ala Ala Ser Phe Gln Arg
20 25 30

Asn Gln Leu Leu Gln Lys Glu Pro Asp Leu Arg Leu Glu Asn Val Gln
35 40 45

Lys Phe Pro Ser Pro Glu Met Ile Arg Ala Leu Glu Tyr Ile Glu Asn
50 55 60

Leu Arg Gln Gln Ala His Lys Glu Glu Ser Ser Pro Asp Tyr Asn Pro
65 70 75 80

Tyr Gln Gly Val Ser Val Pro Leu Gln Gln Lys Glu Asn Gly Asp Glu
85 90 95

Ser His Leu Pro Glu Arg Asp Ser Leu Ser Glu Glu Asp Trp Met Arg
100 105 110

Ile Ile Leu Glu Ala Leu Arg Gln Ala Glu Asn Glu Pro Gln Ser Ala
115 120 125

Pro Lys Glu Asn Lys Pro Tyr Ala Leu Asn Ser Glu Lys Asn Phe Pro
130 135 140

Met Asp Met Ser Asp Asp Tyr Glu Thr Gln Gln Trp Pro Glu Arg
145 150 155